



221749.ST25
SEQUENCE LISTING

<110> GOVERNMENT OF THE UNITED STATES OF AMERICA, REPRESENTED BY
THE SECRETARY, DEPARTMENT OF HEALTH AND HUMAN SERVICES
KAYE, FREDERIC J.
KOMIYA, TAKEFUMI

<120> COMPOSITIONS AND METHODS FOR INHIBITING TRANSLATION OF A CHIMERIC
GENE

<130> 221749

<140> 10/698,070
<141> 2003-10-30

<160> 12

<170> PatentIn version 3.3

<210> 1
<211> 3763
<212> DNA
<213> Homo sapiens

<400> 1
agggtggcggc gagaagatgg cgacttcgaa caatccgcgg aaattcagcg agaagatcgc 60
gctgcacaat cagaagcagg cggaggagac ggccgccttc gaggaggtca tgaaggacct 120
gagcctgacg cggccgcgc ggctccaggg ttcccttggaaa agaaaaacagg tagttaacct 180
atctcctgcc aacagcaagc gacccaatgg ctttgtggac aactcatttc ttgatatcaa 240
aagaattcgt gttggggaga atctctctgc aggacaaggt ggcctccaaa taaacaatgg 300
acaaagttagt attatgtcag ggaccttgcc tatgagccaa gcacccctgc gaaagactaa 360
caactctgcca tcccatacac attctcctgg caatggcctg tttaacatgg gcttaaagga 420
ggtaaagaag gagccaggag agactctgtc ttgcagtaag cacatggatg gccaaatgac 480
ccaagagaat attttccta ataggtacgg agacgaccct ggagaacaac tgatggatcc 540
tgagctgcag gaactgttca atgaactgac caacatatct gtgcctccca tgagtgaccc 600
tgaactggag aacatgatca atgccaccat aaagcaggat gacccattt acattgactt 660
gggtcagcaa agccagagga gcacacctag gccctcctta cccatggaga aaatagtgtat 720
caaaaagtgaa tactcaccgg gcttgactca gggccctca ggctctccctc agctgaggcc 780
ccccatcagct ggcccccgcatt tctccatggc caactctgcc ctctccactt cgtctccaaat 840
cccttcagtc cctcagagcc aggctcagcc tcagacaggc tccggagcaa gccggccctt 900
gccaagctgg caggaagtat cccatccccca gcagctaaaa cagatagctg ctaatcgtca 960
gcagcatgcc cggatgcagc agcaccagca gcagcaccag cctaccaact ggtcagccctt 1020
gccctcctct gctggaccat caccaggtcc atttgggcag gagaaaaatcc ccagcccttc 1080
ttttggtcag cagacattca gcccacagag ctccccatg cctggggtag ctggcggcag 1140

221749.ST25

cggccagtcg aaagttaatgg ctaactacat gtacaaggcc ggcccctcag cccagggtgg	1200
gcacctagat gtcctcatgc agcaaaagcc tcaggatctc agtcgaagtt ttattaacaa	1260
cccgcaccca gccatggagc cccgtcaggg caacaccaag cctttgttc attttaactc	1320
agatcaagcg aaccagcaga tgccttctgt tttgccttcc cagaacaagc cttctctcct	1380
acactacacc caacagcaac agcagcaaca gcagcagcag cagcagcagc agcagcagca	1440
acagcagcag cagcagcaac agcaacagca acagcaacag cagagttcaa tttcagctca	1500
acaacagcaa cagcagcaga gctcaatttc agcccaacag cagcagcagc agcaacaaca	1560
gcagcagcag cagcaacaac aacagcaaca acagcagcag cagcagcagc aacaaccatc	1620
ttctcagcct gcccaatctc taccaagcca gccttgcta aggtcacctt tgccacttca	1680
gaaaaagctc ctacttcagc aaatgcagaa tcagcccatt gcaggaatgg gataccaagt	1740
ctcccaacaa cagagacagg atcaacactc tgtggtaggc cagaacacag gccccagtcc	1800
aagtccctaac ccctgctcaa atccaaacac tggaaagtggt tacatgaact cccagcaatc	1860
actgttgaat cagcaattga tggaaagaa gcagactcta cagaggcaga tcatggagca	1920
gaaacagcaa cttcttctcc agcagcagat gctggctgac gcggagaaaa ttgctccaca	1980
agatcagata aaccgacatt tgtcaaggcc acctccagat tataaagacc aaagaagaaa	2040
tgtggcaat atgcaaccaa ctgctcagta ttctggtggc tcatccacaa taagcttaaa	2100
ctctaaccag gcttggcaa acccagtttc aacacacacc attttaactc ccaattccag	2160
cctcctgtct acttctcagc ggacaagaat gccatcatta tctacagcag ttcagaatat	2220
ggggatgtat ggaaatctgc cttgtaatca acctaacaca tacagtgtca cttcaggaat	2280
gaatcaattg acccaacaga gaaacccaaa gcaattgtta gcaaataaaa acaaccstat	2340
gatgccacgg ccacctacct tagggccaag taataataac aatgtagcca cttttggagc	2400
tggatctgtt ggtaattcac aacaatttag tagggccaag taataataac aatgtagcca cttttggagc	2460
gccaccacag agaacatcaa acgtaatgat cacatccaac acaactgcac caaactggc	2520
ctctcaagaa ggaacaagca aacagcaaga agccctgacg tctgcaggag tccgcttccc	2580
cacaggtaca cctgcagcct atacccaaa tcagtcactg caacaggcag taggtagcca	2640
gcaattttcc cagagggcag tggctcctcc taaccagttt acaccagcag tgcaaataat	2700
acccatgaac caaatgagcc aaacactaaa tggccaaacc atgggtcccc tcaggggtct	2760
gaatctcaga cccaatcagc taagcacaca gatttgcct aatttgaatc agtcaggaac	2820
agggttgaat cagtcgagga cgggcatcaa ccagccacca tccctgacgc ccagcaattt	2880
tccttcaccc aaccaaagtt ccaggcttt tcaaggaact gaccacagca gtgacttagc	2940
ttttgacttc ctcagccaac aaaatgataa catggccctt gcccataaca gtgatgctga	3000
tttcattgat tctttattga agacagagcc tggtaatgat gactggatga aagacatcaa	3060

221749.ST25

tcttgatgaa atcttgggaa acaattccta aagaagaaaag ggaagacaat ttacaaactc	3120
caagcactaa aaggcagtat attacagaaa ctctgttagag gctgaactgt tgatgttcag	3180
gtggactaca tgaagataac atgcttaaaa atggaaagca gaaagtaact gcagtgtga	3240
acattttgtt ccaaattctt gttttaaatc ttacacctga aagtaaaata ttgggatcac	3300
ttttccctgt ctaaactcca ggatacagta tccaatttat ccaaacagaa ctgtgggtgc	3360
aatgtgtaat taattgtgtaaatagcctt cccaagtttc ttttccctg gaaaataaaaa	3420
aaggtaatag aacttgttagt ttatttaaac cccatgtcat gaggaggtac tagttccaag	3480
caacaaactc cttaatttgc tctaatacgat aggtatggtt taatcttcc attgtgtctt	3540
ttcatttaat tttcctgaag cttgcaggat agattgaaat gttataggtt tgtttggagt	3600
aaccaaacag tatgcaaatt aagaaaaagc cagagaacct agaaaacatc cagtggatta	3660
cagaatttct tccccatatt cactcctcac ttttacaatt ttcccacaat cctctacttc	3720
agtggatgc tgtgtctagt gattaaacaa aaatatagag ctg	3763

<210> 2
<211> 73
<212> DNA
<213> Unknown

<220>
<223> RNAi clone

<400> 2 ttggcaggag ataggtaac tacctgttga agcttgagca ggtggtaat ctatctcctg	60
ctaacagttt ttt	73

<210> 3
<211> 71
<212> DNA
<213> Unknown

<220>
<223> RNAi clone

<400> 3 atgtgcagcg cgatcttctc gctgaatgaa gcttgattcg gcgagaaggt cgcgttgcac	60
gatcagtttt t	71

<210> 4
<211> 78
<212> DNA
<213> Unknown

<220>
<223> RNAi clone - antisense

<400> 4

	221749.ST25	
gatcaaaaaa ctgatcggtgc aacgcgacct tctgccgaat caagttcat tcagcgagaa	60	
gatcgcgctg cacaatcg	78	
<210> 5		
<211> 28		
<212> DNA		
<213> Unknown		
<220>		
<223> fragment of Mect1-MAML2 sequence		
<400> 5		
ttggcaggag ataggttaac tacctgtt	28	
<210> 6		
<211> 28		
<212> DNA		
<213> Unknown		
<220>		
<223> fragment of Mect1-MAML2 sequence		
<400> 6		
atttgtcagc gcgatcttct cgctgaat	28	
<210> 7		
<211> 28		
<212> DNA		
<213> Unknown		
<220>		
<223> fragment of Mect1-MAML2 sequence		
<400> 7		
attcagcgag aagatcgcgc tgcacaac	28	
<210> 8		
<211> 19		
<212> RNA		
<213> Unknown		
<220>		
<223> siRNA #1		
<400> 8		
ccuaucuccu gccaacagc	19	
<210> 9		
<211> 19		
<212> RNA		
<213> Unknown		
<220>		
<223> complement to siRNA #1		
<400> 9		
gcuguuggca ggagauagg	19	

221749.ST25

<210> 10
<211> 19
<212> RNA
<213> Unknown

<220>
<223> siRNA #2

<400> 10
cagguaguua accuaucuc

19

<210> 11
<211> 19
<212> RNA
<213> Unknown

<220>
<223> complement to siRNA #2

<400> 11
gagauagguu aacuaccug

19

<210> 12
<211> 1024
<212> PRT
<213> Homo sapiens

<400> 12

Met Ala Thr Ser Asn Asn Pro Arg Lys Phe Ser Glu Lys Ile Ala Leu
1 5 10 15

His Asn Gln Lys Gln Ala Glu Glu Thr Ala Ala Phe Glu Glu Val Met
20 25 30

Lys Asp Leu Ser Leu Thr Arg Ala Ala Arg Leu Gln Gly Ser Leu Lys
35 40 45

Arg Lys Gln Val Val Asn Leu Ser Pro Ala Asn Ser Lys Arg Pro Asn
50 55 60

Gly Phe Val Asp Asn Ser Phe Leu Asp Ile Lys Arg Ile Arg Val Gly
65 70 75 80

Glu Asn Leu Ser Ala Gly Gln Gly Gly Leu Gln Ile Asn Asn Gly Gln
85 90 95

Ser Gln Ile Met Ser Gly Thr Leu Pro Met Ser Gln Ala Pro Leu Arg
100 105 110

Lys Thr Asn Thr Leu Pro Ser His Thr His Ser Pro Gly Asn Gly Leu
115 120 125

221749.ST25

Phe Asn Met Gly Leu Lys Glu Val Lys Lys Glu Pro Gly Glu Thr Leu
130 135 140

Ser Cys Ser Lys His Met Asp Gly Gln Met Thr Gln Glu Asn Ile Phe
145 150 155 160

Pro Asn Arg Tyr Gly Asp Asp Pro Gly Glu Gln Leu Met Asp Pro Glu
165 170 175

Leu Gln Glu Leu Phe Asn Glu Leu Thr Asn Ile Ser Val Pro Pro Met
180 185 190

Ser Asp Leu Glu Leu Glu Asn Met Ile Asn Ala Thr Ile Lys Gln Asp
195 200 205

Asp Pro Phe Asn Ile Asp Leu Gly Gln Gln Ser Gln Arg Ser Thr Pro
210 215 220

Arg Pro Ser Leu Pro Met Glu Lys Ile Val Ile Lys Ser Glu Tyr Ser
225 230 235 240

Pro Gly Leu Thr Gln Gly Pro Ser Gly Ser Pro Gln Leu Arg Pro Pro
245 250 255

Ser Ala Gly Pro Ala Phe Ser Met Ala Asn Ser Ala Leu Ser Thr Ser
260 265 270

Ser Pro Ile Pro Ser Val Pro Gln Ser Gln Ala Gln Pro Gln Thr Gly
275 280 285

Ser Gly Ala Ser Arg Ala Leu Pro Ser Trp Gln Glu Val Ser His Ala
290 295 300

Gln Gln Leu Lys Gln Ile Ala Ala Asn Arg Gln Gln His Ala Arg Met
305 310 315 320

Gln Gln His Gln Gln His Gln Pro Thr Asn Trp Ser Ala Leu Pro
325 330 335

Ser Ser Ala Gly Pro Ser Pro Gly Pro Phe Gly Gln Glu Lys Ile Pro
340 345 350

Ser Pro Ser Phe Gly Gln Gln Thr Phe Ser Pro Gln Ser Ser Pro Met
355 360 365

Pro Gly Val Ala Gly Gly Ser Gly Gln Ser Lys Val Met Ala Asn Tyr

221749.ST25

370

375

380

Met Tyr Lys Ala Gly Pro Ser Ala Gln Gly Gly His Leu Asp Val Leu
385 390 395 400

Met Gln Gln Lys Pro Gln Asp Leu Ser Arg Ser Phe Ile Asn Asn Pro
405 410 415

His Pro Ala Met Glu Pro Arg Gln Gly Asn Thr Lys Pro Leu Phe His
420 425 430

Phe Asn Ser Asp Gln Ala Asn Gln Gln Met Pro Ser Val Leu Pro Ser
435 440 445

Gln Asn Lys Pro Ser Leu Leu His Tyr Thr Gln Gln Gln Gln Gln Gln
450 455 460

Gln
465 470 475 480

Gln Gln Gln Gln Gln Gln Gln Ser Ser Ile Ser Ala Gln Gln
485 490 495

Gln Gln Gln Gln Gln Ser Ser Ile Ser Ala Gln Gln Gln Gln Gln Gln
500 505 510

Gln
515 520 525

Gln Gln Gln Gln Gln Pro Ser Ser Gln Pro Ala Gln Ser Leu Pro Ser
530 535 540

Gln Pro Leu Leu Arg Ser Pro Leu Pro Leu Gln Gln Lys Leu Leu Leu
545 550 555 560

Gln Gln Met Gln Asn Gln Pro Ile Ala Gly Met Gly Tyr Gln Val Ser
565 570 575

Gln Gln Gln Arg Gln Asp Gln His Ser Val Val Gly Gln Asn Thr Gly
580 585 590

Pro Ser Pro Ser Pro Asn Pro Cys Ser Asn Pro Asn Thr Gly Ser Gly
595 600 605

Tyr Met Asn Ser Gln Gln Ser Leu Leu Asn Gln Gln Leu Met Gly Lys
610 615 620

221749.ST25

Lys Gln Thr Leu Gln Arg Gln Ile Met Glu Gln Lys Gln Gln Leu Leu
625 630 635 640

Leu Gln Gln Gln Met Leu Ala Asp Ala Glu Lys Ile Ala Pro Gln Asp
645 650 655

Gln Ile Asn Arg His Leu Ser Arg Pro Pro Pro Asp Tyr Lys Asp Gln
660 665 670

Arg Arg Asn Val Gly Asn Met Gln Pro Thr Ala Gln Tyr Ser Gly Gly
675 680 685

Ser Ser Thr Ile Ser Leu Asn Ser Asn Gln Ala Leu Ala Asn Pro Val
690 695 700

Ser Thr His Thr Ile Leu Thr Pro Asn Ser Ser Leu Leu Ser Thr Ser
705 710 715 720

His Gly Thr Arg Met Pro Ser Leu Ser Thr Ala Val Gln Asn Met Gly
725 730 735

Met Tyr Gly Asn Leu Pro Cys Asn Gln Pro Asn Thr Tyr Ser Val Thr
740 745 750

Ser Gly Met Asn Gln Leu Thr Gln Gln Arg Asn Pro Lys Gln Leu Leu
755 760 765

Ala Asn Gln Asn Asn Pro Met Met Pro Arg Pro Pro Thr Leu Gly Pro
770 775 780

Ser Asn Asn Asn Asn Val Ala Thr Phe Gly Ala Gly Ser Val Gly Asn
785 790 795 800

Ser Gln Gln Leu Arg Pro Asn Leu Thr His Ser Met Ala Ser Met Pro
805 810 815

Pro Gln Arg Thr Ser Asn Val Met Ile Thr Ser Asn Thr Thr Ala Pro
820 825 830

Asn Trp Ala Ser Gln Glu Gly Thr Ser Lys Gln Gln Glu Ala Leu Thr
835 840 845

Ser Ala Gly Val Arg Phe Pro Thr Gly Thr Pro Ala Ala Tyr Thr Pro
850 855 860

Asn Gln Ser Leu Gln Gln Ala Val Gly Ser Gln Gln Phe Ser Gln Arg
865 870 875 880

221749.ST25

Ala Val Ala Pro Pro Asn Gln Leu Thr Pro Ala Val Gln Met Arg Pro
885 890 895

Met Asn Gln Met Ser Gln Thr Leu Asn Gly Gln Thr Met Gly Pro Leu
900 905 910

Arg Gly Leu Asn Leu Arg Pro Asn Gln Leu Ser Thr Gln Ile Leu Pro
915 920 925

Asn Leu Asn Gln Ser Gly Thr Gly Leu Asn Gln Ser Arg Thr Gly Ile
930 935 940

Asn Gln Pro Pro Ser Leu Thr Pro Ser Asn Phe Pro Ser Pro Asn Gln
945 950 955 960

Ser Ser Arg Ala Phe Gln Gly Thr Asp His Ser Ser Asp Leu Ala Phe
965 970 975

Asp Phe Leu Ser Gln Gln Asn Asp Asn Met Gly Pro Ala Leu Asn Ser
980 985 990

Asp Ala Asp Phe Ile Asp Ser Leu Leu Lys Thr Glu Pro Gly Asn Asp
995 1000 1005

Asp Trp Met Lys Asp Ile Asn Leu Asp Glu Ile Leu Gly Asn Asn
1010 1015 1020

Ser